

FIGURE 1

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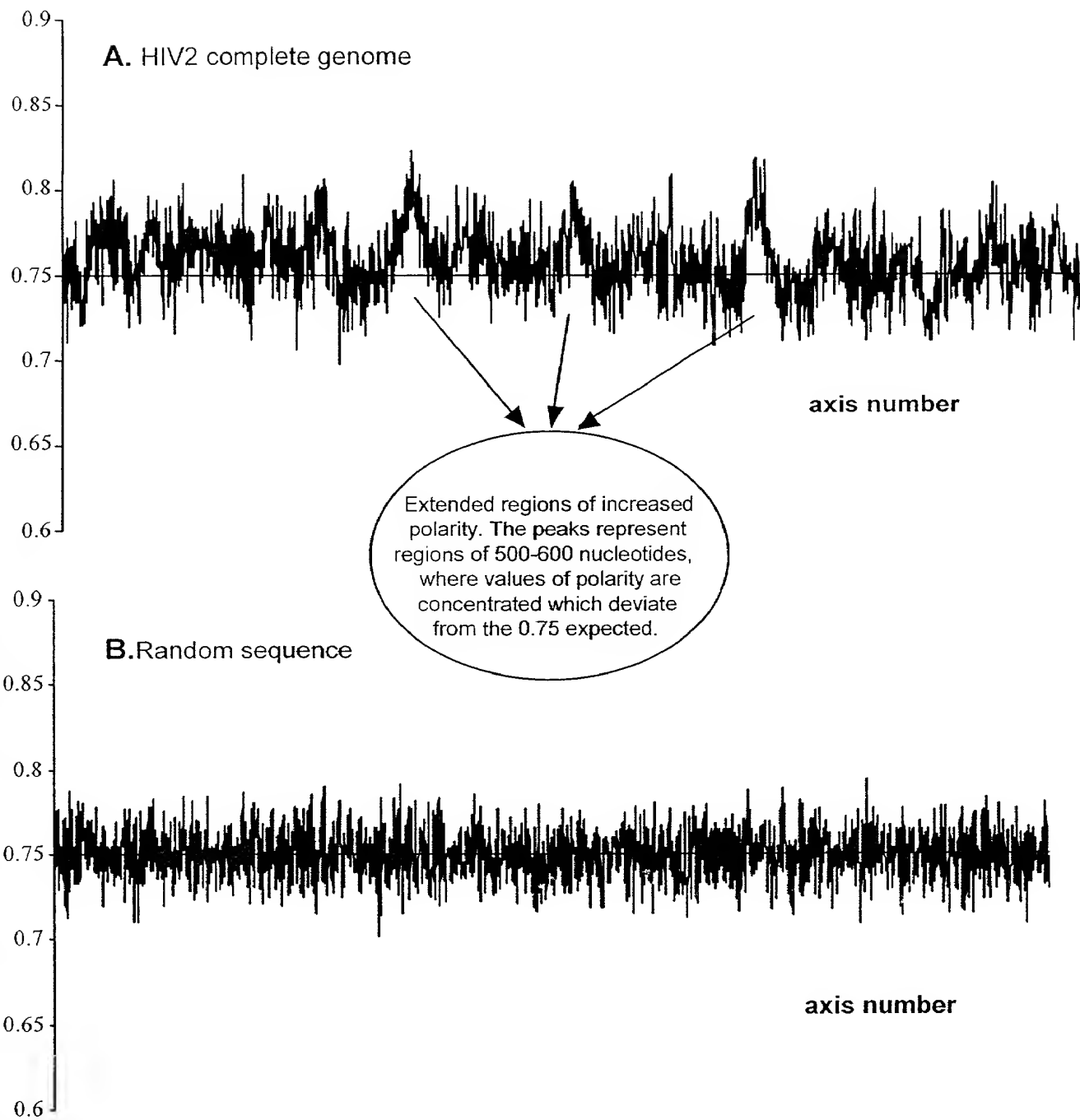
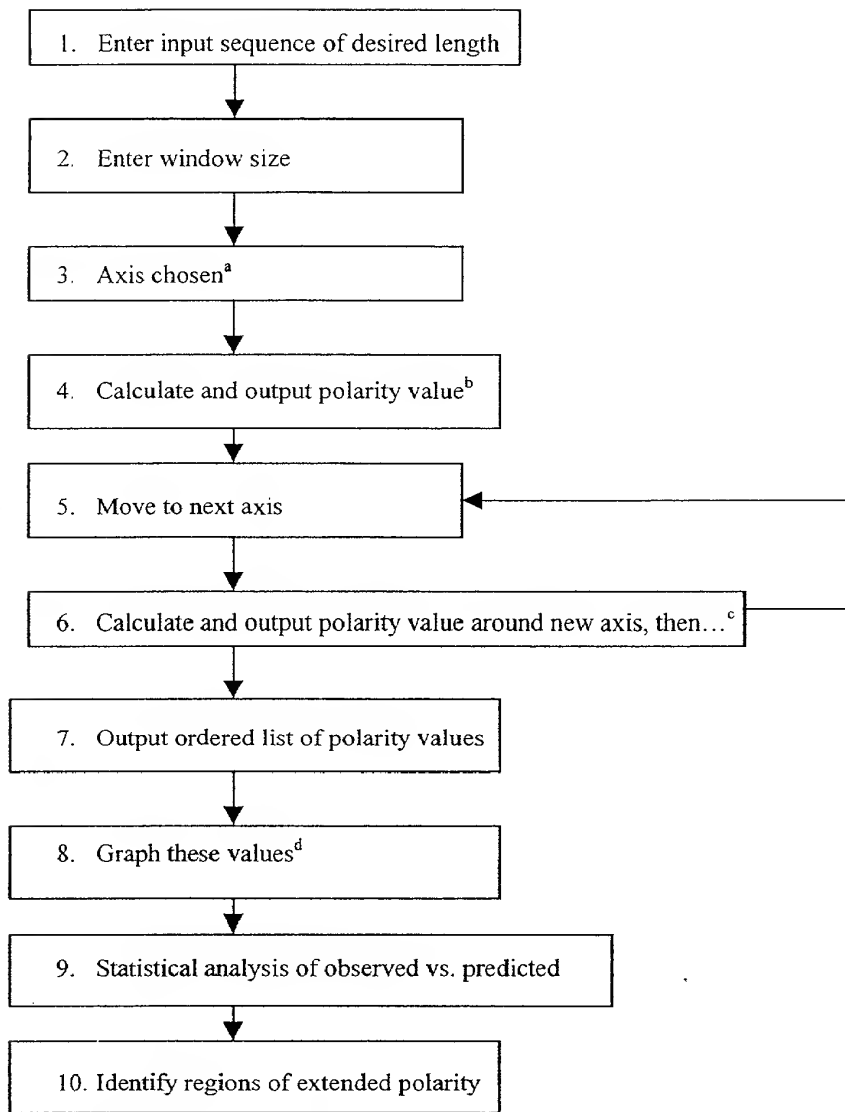


FIGURE 2



^a Starting at position = $(2 * \text{window of symmetry})$

^b $[1 - (S/W)]$

^c Up to and including axis position = $[2 * \text{length} - (2 * \text{window size})]$

^d Can use a moving average of values (with number of values averaged and increment of moving being variable) to smooth curve

FIGURE 3

The algorithm was implemented in PERL programming language
 PERL variable-names and function-names are in boldface.

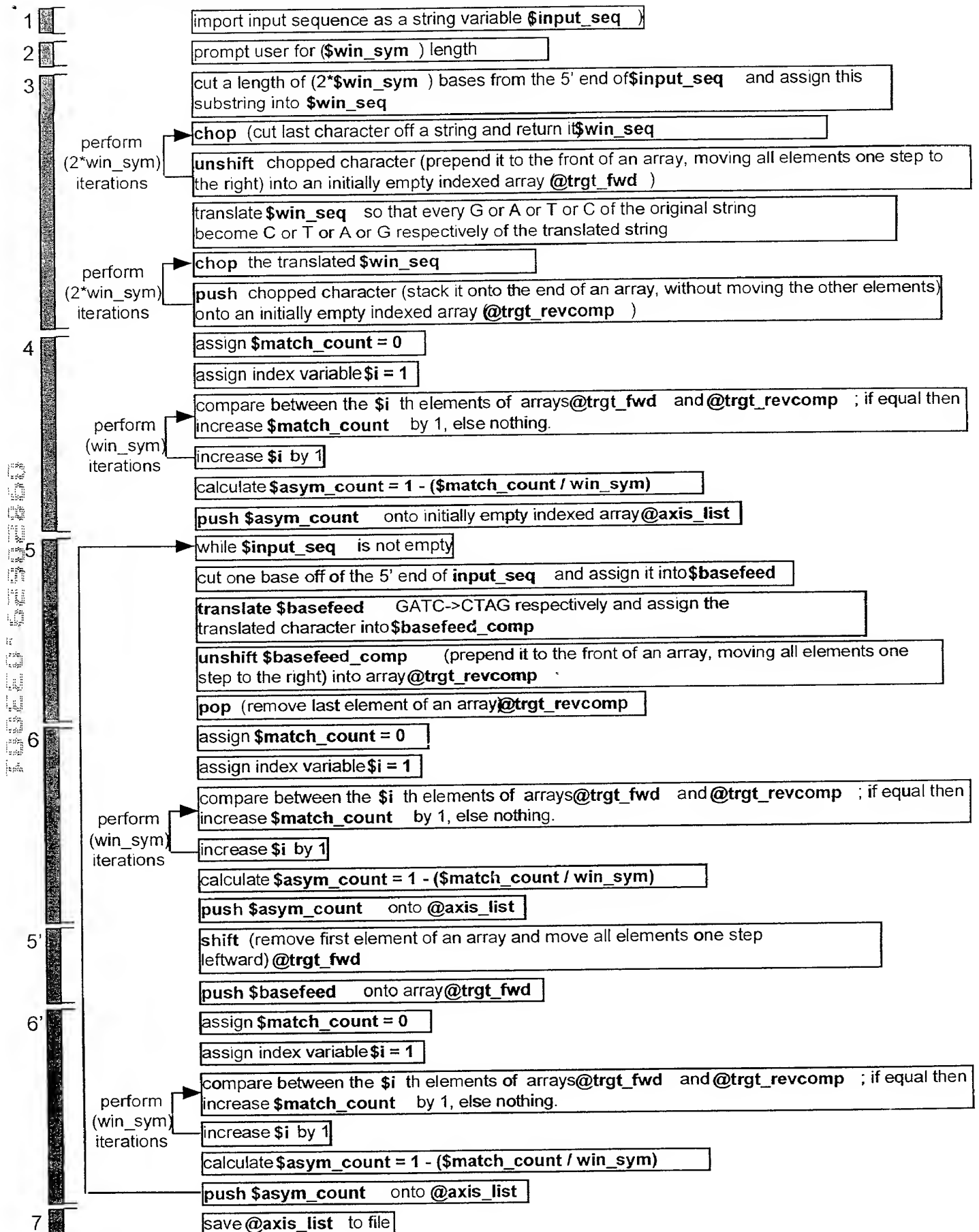
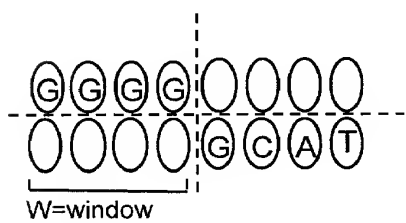


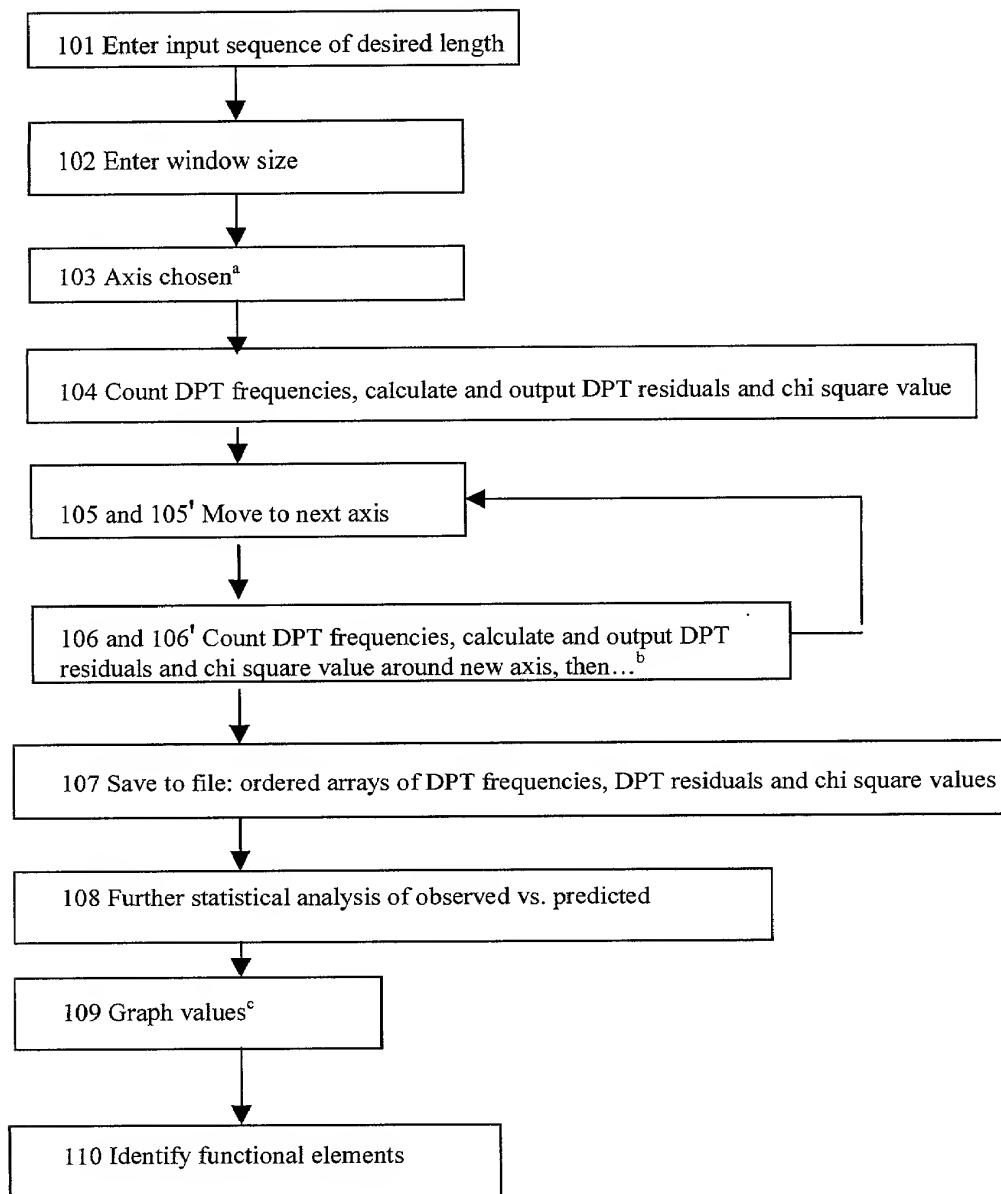
FIGURE 4

self dyad	self mirror	Purine pyrimidine dyad	Purine pyrimidine mirror
i=1: G--G	i=5: G--C	i=9: G--A	i=13: G--T
i=2: A--A	i=6: A--T	i=10: A--G	i=14: A--C
i=3: T--T	i=7: T--A	i=11: T--C	i=15: T--G
i=4: C--C	i=8: C--G	i=12: C--T	i=16: C--A

↑
Figure 5A

Figure 5B





^a Starting at axis position = $(2 * \text{window size})$

^b Up to and including axis position = $[2 * \text{length} - (2 * \text{window size})]$

^c Values include DPT frequencies, statistical measures including residuals and χ^2

FIGURE 6

The algorithm was implemented in PERL programming language.
PERL variable-names and function-names are in boldface.

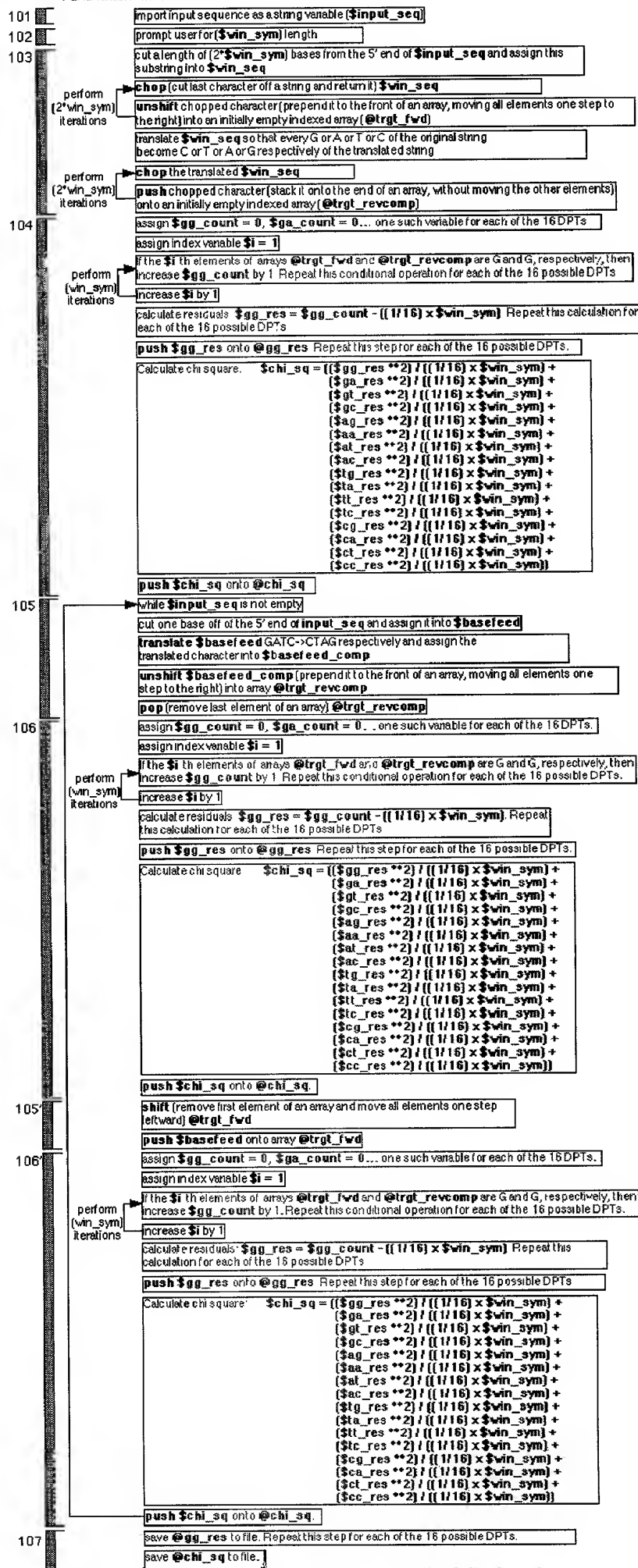


FIGURE 7

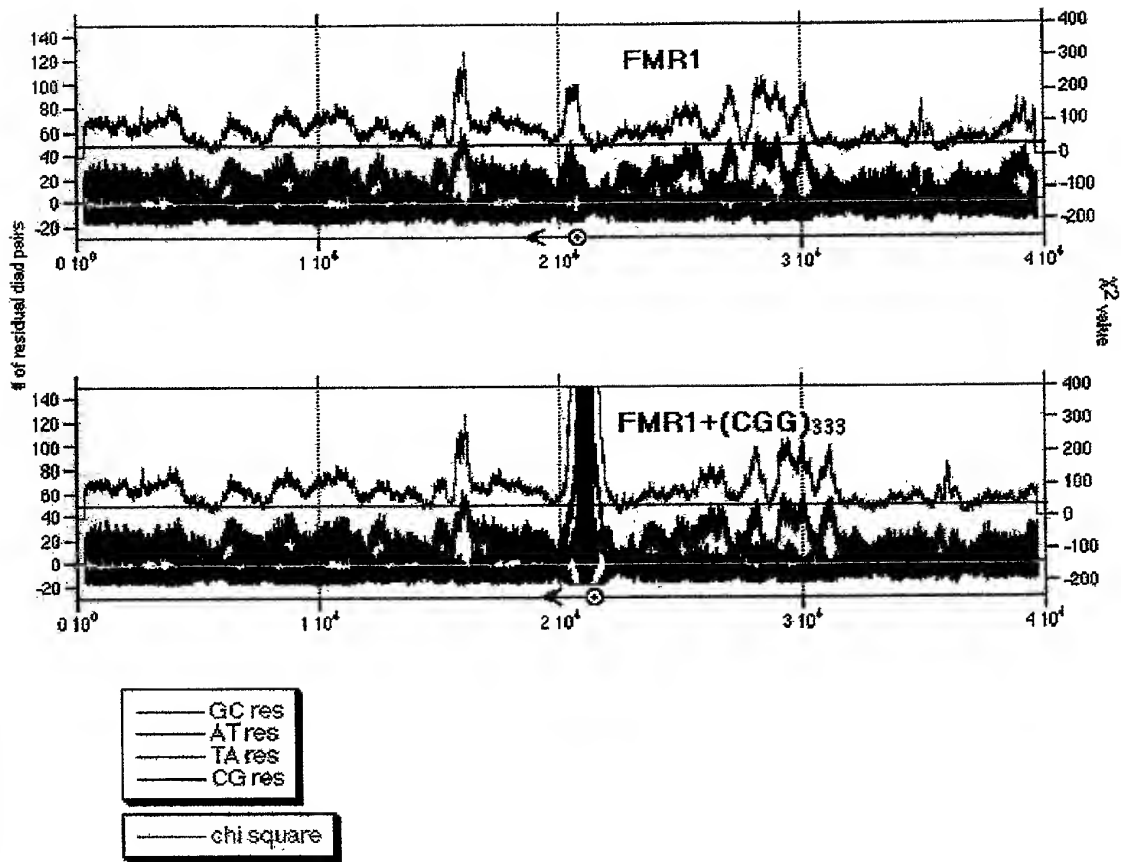


FIGURE 9

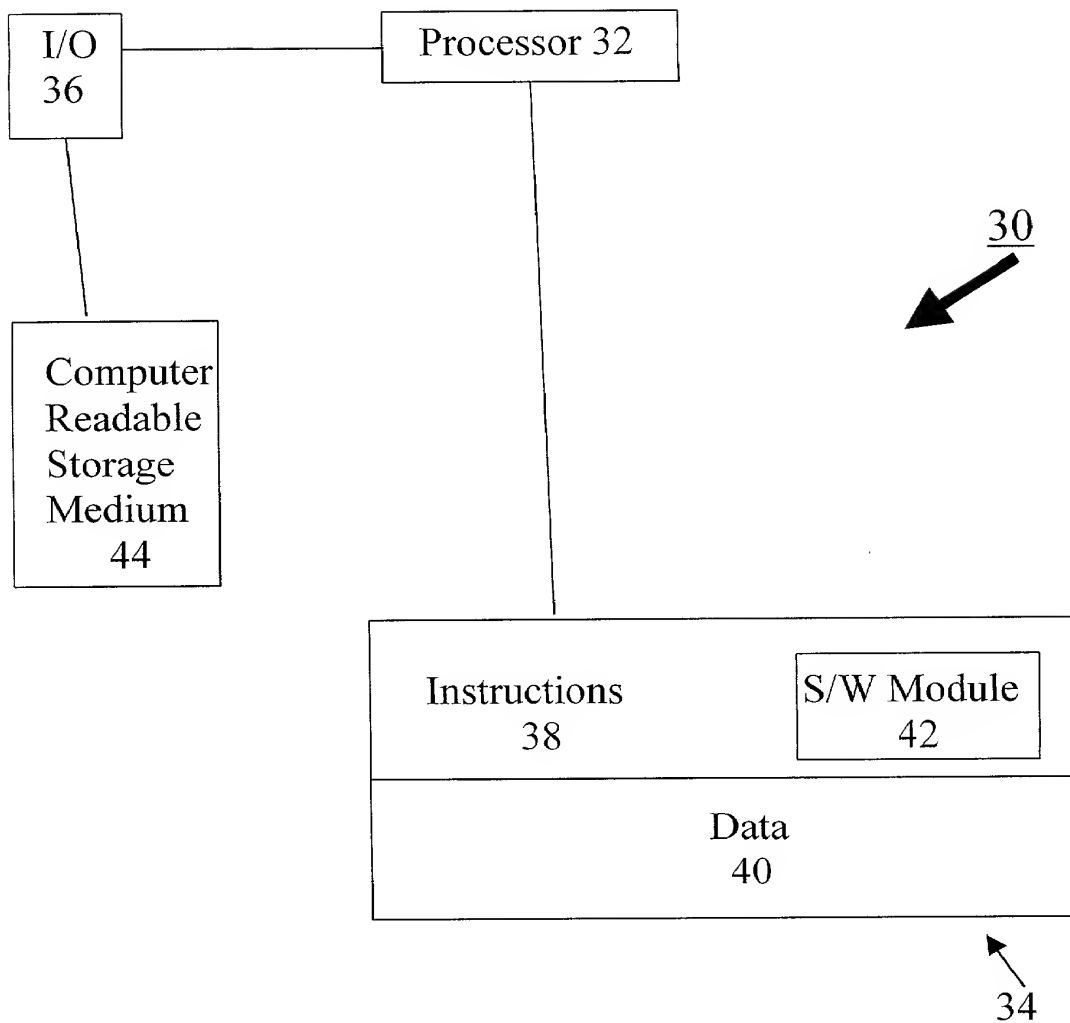


FIGURE 10